

FIG. 1

1 CTCTAGATGTACATGGAGGATGACCGAAAAACCAATGGTGTGAAGAGCTCCCCAGCCAA 60
 1 M T E K T N G V K S S P A N 14
 61 TAATCACAACCATCATGCACCTCCTGCCATCAAGGCCAATGGCAAAGATGACCACAGGAC 120
 15 N H N H H A P P A I K A N G K D D H R T 34
 121 AAGCAGCAGGCCACACTCTGCAGCTGACGATGACACCTCCTCAGAACTGCAGAGGCTGGC 180
 35 S S R P H S A A D D D T S S E L Q R L A 54
 181 AGACGTGGATGCCCCACAGCAGGGAAGGAGTGGCTTCCGCAGGATAGTTCGCCTGGTGGG 240
 55 D V D A P Q Q G R S G F R R I V R L V G 74
 241 GATCATCAGAGAATGGGCCAACCAAGAATTTCCGAGAGGAGGAACCTAGGCCTGACTCATT 300
 75 I I R E W A N K N F R E E E P R P D S F 94
 301 CCTCGAGCGTTTTCTGTGGGCCTGAACCTCAGACTGTGACCACACAGGAGGGGGATGGCAA 360
 95 L E R F R G P E L Q T V T T Q E G D G K 114
 361 AGGCGACAAGGATGGCGAGGACAAAGGCACCAAGAAGAAATTTGAACTATTTGTCTTGGA 420
 115 G D K D G E D K G T K K K F E L F V L D 134
 421 CCCAGCTGGGGATTTGTACTACTGCTGGCTATTTGTCTATTGCCATGCCGTCCTTTACAA 480
 135 P A G D L Y Y C W L F V I A M P V L Y N 154
 481 CTGGTGCCTGCTGGTGGCCAGAGCCTGCTTCAGTGACCTACAGAAAGGCTACTACCTGGT 540
 155 W C L L V A R A C F S D L Q K G Y Y L V 174
 541 GTGGCTGGTGTGGATTATGTCTCAGATGTGGTCTACATTGCGGACCTCTTCATCCGATT 600
 175 W L V L D Y V S D V V Y I A D L F I R L 194
 601 GCGCACAGGTTTCTGGAGCAGGGGCTGCTGGTCAAAGATACCAAGAACTGCGAGACAA 660
 195 R T G F L E Q G L L V K D T K K L R D N 214
 661 CTACATCCACACCCTGCAGTTCAAGCTGGATGTGGCTTCCATCATCCCCACTGACCTGAT 720
 215 Y I H T L Q F K L D V A S I I P T D L I 234
 721 CTATTTTGCTGTGGACATCCACAGCCCTGAGGTGCGCTTCAACCGCTGCTGCACTTTGC 780
 235 Y F A V D I H S P E V R F N R L L H F A 254
 781 CCGCATGTTTGAGTTCTTTGACCGACAGAGACACGCACCAACTACCCTAACATCTTCG 840
 255 R M F E F F D R T E T R T N Y P N I F R 274
 841 CATCAGCAACCTTGTCTCTACATCTTGGTCATCATCCACTGGAATGCCTGCATCTATTA 900
 275 I S N L V L Y I L V I I H W N A C I Y Y 294
 901 TGCCATCTCCAAATCCATAGGCTTTGGGGTCGACACCTGGGTTTACCCAAACATCACTGA 960
 295 A I S K S I G F G V D T W V Y P N I T D 314

FIG. 1 (Cont'd)

961	CCCTGAGTATGGCTACCTGGCTAGGGAATACATCTATTGCCTTTACTGGTCCACACTGAC	1020
315	P E Y G Y L A R E Y I Y C L Y W S T L T	334
1021	TCTCACTACCATTGGGGAGACACCACCCCTGTAAAGGATGAGGAGTACCTATTTGTTCAT	1080
335	L T T I G E T P P P V K D E E Y L F V I	354
1081	CTTTGACTTCCTGATTGGCGTCCTCATCTTTGCCACCATCGTGGGAAATGTGGGCTCCAT	1140
355	F D F L I G V L I F A T I V G N V G S M	374
1141	GATCTCCAACATGAATGCCACCCGGGCAGAGTTCAGGCTAAGATCGATGCCGTGAAACA	1200
375	I S N M N A T R A E F Q A K I D A V K H	394
1201	CTACATGCAGTTCCGAAAGGTGAGCAAGGGGATGGAAGCCAAGGTCATTAGGTGGTTTGA	1260
395	Y M Q F R K V S K G M E A K V I R W F D	414
1261	CTACTTGTGGACCAATAAGAAGACAGTGGATGAGCGAGAAATTCTCAAGAATCTGCCAGC	1320
415	Y L W T N K K T V D E R E I L K N L P A	434
1321	CAAGCTCAGGGCTGAGATAGCCACCAATGTCCACTTGTCCACACTCAAGAAAGTGCGCAT	1380
435	K L R A E I A T N V H L S T L K K V R I	454
1381	CTTCCATGATTGTGAGGCTGGCCTGCTGGTAGAGCTGGTACTGAAACTCCGTCCTCAGGT	1440
455	F H D C E A G L L V E L V L K L R P Q V	474
1441	CTTCAGTCCTGGGGATTACATTTGCCGCAAAGGGGACATCGGCAAGGAGATGTACATCAT	1500
475	F S P G D Y I C R K G D I G K E M Y I I	494
1501	TAAGGAGGGCAAAGTGGCAGTGGTGGCTGATGATGGTGTGACTCAGTATGCTCTGCTGTC	1560
495	K E G K L A V V A D D G V T Q Y A L L S	514
1561	GGCTGGAAGCTGCTTTGGCGAGATCAGTATCCTTAACATTAAGGGCAGTAAAATGGGCAA	1620
515	A G S C F G E I S I L N I K G S K M G N	534
1621	TCGACGCACAGCTAATATCCGCAGCCTGGGCTACTCAGATCTCTTCTGCTGTGCAAGGA	1680
535	R R T A N I R S L G Y S D L F C L S K D	554
1681	TGATCTTATGGAAGCTGTGACTGAGTACCCTGATGCCAAGAAAGTCTAGAAAGAGAGGGG	1740
555	D L M E A V T E Y P D A K K V L E E R G	574
1741	TCGGGAGATCCTCATGAAGGAGGGACTGCTGGATGAGAACGAAGTGGCAACCAGCATGGA	1800
575	R E I L M K E G L L D E N E V A T S M E	594
1801	GGTCGACGTGCAGGAGAAGCTAGGGCAGCTGGAGACCAACATGGAACCTTGTACACTCG	1860
595	V D V Q E K L G Q L E T N M E T L Y T R	614
1861	CTTTGGCCGCTGCTGGCTGAGTACCGGGGGCCAGCAGAAGCTCAAGCAGCGCATCAC	1920
615	F G R L L A E Y T G A Q Q K L K Q R I T	634

FIG. 1 (Cont'd)

1921 AGTTCTGGAAACCAAGATGAAACAGAACAAATGAAGATGACTACCTGTCTGATGGGATGAA 1980
635 V L E T K M K Q N N E D D Y L S D G M N 654

1981 CAGCCCTGAGCTGGCTGCTGCTGACGAGCCATAAGACCTGGGGCCCAACTGCCTCTCCAG 2040
655 S P E L A A A D E P 664

2041 CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTTAGATCTCCGGATTACAT 2100

2101 GCATTACCCTCATGTTCCCTGAATTCTCCAAAAGTCTCTCTGACCCTGNGTTTTTGGCC 2160

2161 TAAACATCCAAGATCCGCCTCGGAT 2186

1921 AGTTCTGGAAACCAAGATGAAACAGAACAAATGAAGATGACTACCTGTCTGATGGGATGAA 1980
635 V L E T K M K Q N N E D D Y L S D G M N 654

1981 CAGCCCTGAGCTGGCTGCTGCTGACGAGCCATAAGACCTGGGGCCCAACTGCCTCTCCAG 2040
655 S P E L A A A D E P 664

2041 CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTTAGATCTCCGGATTACAT 2100

2101 GCATTACCCTCATGTTCCCTGAATTCTCCAAAAGTCTCTCTGACCCTGNGTTTTTGGCC 2160

2161 TAAACATCCAAGATCCGCCTCGGAT 2186

FIG. 2

MTEKTNGVKSSPANNHNNHAPPAIKANGKDDHRTSSRPHSAADDDTSSELQRLADVDAPQQGRSGFERRI
VRLVGIIREWANKNFREEEPRPDSFLERFRGPELQTVTTQEGDGKGDGEDKGTKKKFELFVLDPAGD
LYYCWLFIAMPVLYNWCLLVARACFSDLQKGYLLVWLVLVDYVSDVVIADLFIRLRTGFLEQGLLVKD
TKKLRDNYIHTLQFKLDVASIIPDLYFAVDIHSPEVRFNRLLHFARMFEFFDRTETRTNYPNIFRIS
NLVLYILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTTLTTIGETPPPV
KDEEYLFVIFDFLIGVLIFATIVGNVGSISMNATRAEFQAKIDAVKHVMQFRKVSKEAKVIRWFD
YLWTNKKTVDEREILKNLPAKLRAEIATNVHLSTLKKVRIFHDCEAGLLVELVLKLRPQVFSPGDYICR
KGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKSGSKMGNRRRTANIRSLGYSDFCLS
KDDLMEAVTEYPDAAKVLLEERGREILMKEGLLDENEVATSMEVDVQEKLGQLETNMETLYTRFGRLLAE
YTGAQQKLKQRITVLETKMKQNNEDDYLSGDMNSPELAAADEP

FIG. 3

MTEKTNGVKSSPANNHNNHHAPPAIKANGKDDHRTSSRPHSAADDDTSSELQRLADVDPQQGRSGFRR
VRLVGIIREWANKNFREEEPDPDSFLERFRGPQLQTVTTQEGDGKGDGEDKGTKKKFELFVLD PAGD
LYYCWLFEVIAMPVLYNWCLLVARACFSDLQKGYLVWLVLVDYVSDVVYIADLFIRLRTGFLEQGGLLVKD
TKKLRDNYIHTLQFKLDVASIIPDLYFAVDIHSPEVRFNRLHFARMFEFFDRTETRTNYPNIFRIS
NLVLYILVYIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTTLTTIGETPPPV
KDEEYLFVIFDFLIGVLIFATIVGNVGSMSNMNATRAEFQAKIDAVKHVMQFRKVS KGMEAKVIRWFD
YLWTKKTVDEREILKNLPAKLRAEIATNVHLSTLKKVRIFHDCEAGLLVELVLKLRPQVFS PGDYICR
KGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKSGMGNRRRTANIRSLGYSDLFCLS
KDDLMEAVTEYPDAAKVLLEERGRIILMKEGLLDENEVATSMEVDVQEKLGQLETNMETLYTRFGRLAE
YTGAQQKLKQRITVLETKMKQNNEDDYLSDGMNSPELAAADEP

FIG. 4

			1		50
HBYCNG	(1)		-----		
CNG2_BOS	(1)		-----		
CNG2_MOUSE	(1)		-----		
CNG2_RAT	(1)		-----		
rACNG	(1)		MSSWRSCARAPLSGSAWRRSAATRRSRRCLKTKRKRWSSGKGTQMSTQC		
			51		100
HBYCNG	(1)		-----	MTEK	NGVKSSPANNHNNHAPPATKANGKDDH
CNG2_BOS	(1)		-----	MTEK	ANGVKSSPANNHNNHAPPATKANGKDDH
CNG2_MOUSE	(1)		-----	MMTEK	SNGVKSSPANNHNNHPPSTKANGKDDH
CNG2_RAT	(1)		-----	MMTEK	SNGVKSSPANNHNNHPPSTKANGKDDH
rACNG	(51)		ETRRRAQTPCESTGHTWR	MMTEK	SNGVKSSPANNHNNHPPATKANGKDDH
			101		150
HBYCNG	(33)		RTSSRPQ	SAADDDTSSSELQRLA	VDPAQGRSGFRRIVRLVGIRIRWAN
CNG2_BOS	(33)		RASSRPQ	SAADDDTSSSELQRLA	EMDAPOQRGGFRRIVRLVGIRIRWAN
CNG2_MOUSE	(34)		RAGSRPQSV	AADDDTSSSELQRLA	EMDTPRRGRGGFRRIVRLVGIRIRWAN
CNG2_RAT	(34)		RAGSRPQSV	AADDDTSSSELQRLA	EMDTPRRGRGGFRRIVRLVGIRIRWAN
rACNG	(101)		RTSSRPQ	SAADDDTSSSELQRLA	EMDAPOQRGGFRRIVRLVGIRIRWAN
			151		200
HBYCNG	(82)		KNFREEEPRPDSFLERFRGPELQTVTTQ	GDGKGDKDGE	DGKTKKKFELE
CNG2_BOS	(82)		KNFREEEPRPDSFLERFRGPELQTVTTQ	GDGKGDKDGE	DGKTKKKFELE
CNG2_MOUSE	(84)		KNFREEEPRPDSFLERFRGPELQTVTTQ	GDGKGDKDGE	DGKTKKKFELE
CNG2_RAT	(84)		KNFREEEPRPDSFLERFRGPELQTVTTQ	GDGKGDKDGE	DGKTKKKFELE
rACNG	(150)		KNFREEEPRPDSFLERFRGPELQTVTTQ	GDGKGDKDGE	DGKTKKKFELE
			201		250
HBYCNG	(132)		VLDPAGDL	LYCWL	FVIAMPVLYNWCLLVARACFSDLOKGYLVWLVLVDYV
CNG2_BOS	(132)		VLDPAGDWY	YRWLF	IAIPVLYNWCLLVARACFSDLOKGYLVWLVLVDYV
CNG2_MOUSE	(134)		VLDPAGDWY	YRWLF	FVIAMPVLYNWCLLVARACFSDLOKGYLVWLVLVDYV
CNG2_RAT	(134)		VLDPAGDWY	YRWLF	FVIAMPVLYNWCLLVARACFSDLOKGYLVWLVLVDYV
rACNG	(200)		VLDPAGDWY	YRWLF	FVIAMPVLYNWCLLVARACFSDLOKGYLVWLVLVDYV
			251		300
HBYCNG	(182)		SDVVYIADLFIRLRTGFLEQGLLVKD	TKKLRDNYIHTLQFKLDVASI	IPT
CNG2_BOS	(182)		SDVVYIADLFIRLRTGFLEQGLLVKD	TKKLRDNYIHTLQFKLDVASI	IPT
CNG2_MOUSE	(184)		SDIVYIADLFIRLRTGFLEQGLLVKD	PKKLRDNYIHTLQFKLDVASI	IPT
CNG2_RAT	(184)		SDIVYIADLFIRLRTGFLEQGLLVKD	PKKLRDNYIHTLQFKLDVASI	IPT
rACNG	(250)		SDVVYIADLFIRLRTGFLEQGLLVKD	PKKLRDNYIHTLQFKLDVASI	IPT
			301		350
HBYCNG	(232)		DLIYFAVD	IHSPEVRFNRLHFARMFEFFDR	TETRTSYPNIFRISNLVLY
CNG2_BOS	(232)		DLIYFAVG	IHSPEVRFNRLHFARMFEFFDR	TETRTSYPNIFRISNLVLY
CNG2_MOUSE	(234)		DLIYFAVG	IHSPEVRFNRLHFARMFEFFDR	TETRTSYPNIFRISNLVLY
CNG2_RAT	(234)		DLIYFAVG	IHSPEVRFNRLHFARMFEFFDR	TETRTSYPNIFRISNLVLY
rACNG	(300)		DLIYFAVG	IHSPEVRFNRLHFARMFEFFDR	TETRTSYPNIFRISNLVLY
			351		400
HBYCNG	(282)		ILVLIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS		
CNG2_BOS	(282)		ILVLIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS		
CNG2_MOUSE	(284)		ILVLIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS		
CNG2_RAT	(284)		ILVLIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS		
rACNG	(350)		ILVLIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS		

FIG. 4 (Continued)

		401	450
HBMYCNG	(332)	TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGS MISNMNAT	
CNG2_BOS	(332)	TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGS MISNMNAT	
CNG2_MOUSE	(334)	TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGS MISNMNAT	
CNG2_RAT	(334)	TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGS MISNMNAT	
rACNG	(400)	TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGS MISNMNAT	
		451	500
HBMYCNG	(382)	RAEFQAKIDAVKHYMQFRKVSKEAKVIRWFDYLWTNKKTVDEREVLKN	
CNG2_BOS	(382)	RAEFQAKIDAVKHYMQFRKVSKEAKVIRWFDYLWTNKKTVDEREVLKN	
CNG2_MOUSE	(384)	RAEFQAKIDAVKHYMQFRKVSKEAKVIRWFDYLWTNKKTVDEREVLKN	
CNG2_RAT	(384)	RAEFQAKIDAVKHYMQFRKVSKEAKVIRWFDYLWTNKKTVDEREVLKN	
rACNG	(450)	RAEFQAKIDAVKHYMQFRKVSKEAKVIRWFDYLWTNKKTVDEREVLKN	
		501	550
HBMYCNG	(432)	LPAKLRAEIAINVHLSTLKKVRIHQDCEAGLLVELVLKLRPQVFS PGDYI	
CNG2_BOS	(432)	LPAKLRAEIAINVHLSTLKKVRIHQDCEAGLLVELVLKLRPQVFS PGDYI	
CNG2_MOUSE	(434)	LPAKLRAEIAINVHLSTLKKVRIHQDCEAGLLVELVLKLRPQVFS PGDYI	
CNG2_RAT	(434)	LPAKLRAEIAINVHLSTLKKVRIHQDCEAGLLVELVLKLRPQVFS PGDYI	
rACNG	(500)	LPAKLRAEIAINVHLSTLKKVRIHQDCEAGLLVELVLKLRPQVFS PGDYI	
		551	600
HBMYCNG	(482)	CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK	
CNG2_BOS	(482)	CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK	
CNG2_MOUSE	(484)	CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK	
CNG2_RAT	(484)	CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK	
rACNG	(550)	CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK	
		601	650
HBMYCNG	(532)	MGNRRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAAKVLEERGREILMKE	
CNG2_BOS	(532)	MGNRRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAAKVLEERGREILMKE	
CNG2_MOUSE	(534)	MGNRRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAAKVLEERGREILMKE	
CNG2_RAT	(534)	MGNRRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAAKVLEERGREILMKE	
rACNG	(600)	MGNRRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAAKVLEERGREILMKE	
		651	700
HBMYCNG	(582)	GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAAQOKLKQ	
CNG2_BOS	(582)	GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAAQOKLKQ	
CNG2_MOUSE	(584)	GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAAQOKLKQ	
CNG2_RAT	(584)	GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAAQOKLKQ	
rACNG	(650)	GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAAQOKLKQ	
		701	733
HBMYCNG	(632)	RITVLETKMKONHEDDYLS DGMNSPELAAAEPP	
CNG2_BOS	(632)	RITVLETKMKONHEDDYLS DGMNSPEPPAEKP-	
CNG2_MOUSE	(634)	RITVLETKMKONHEDDYLS DGINTP EPAVAE--	
CNG2_RAT	(634)	RITVLETKMKONHEDDYLS DGINTP EPTAAE--	
rACNG	(700)	RITVLETKMKONHEDDYLS DGMNSPEPAAAEQP	

FIG. 5

1 CTCTAGATGTACATGGAGGATGACCGAAAAACCAATGGTGTGAAGAGCTCCCCAGCCAA 60
 1 M T E K T N G V K S S P A N 14
 61 TAATCACAACCATCATGCACCTCCTGCCATCAAGGCCAATGGCAAAGATGACCACAGGAC 120
 15 N H N H H A P P A I K A N G K D D H R T 34
 121 AAGCAGCAGGCCACACTCTGCAGCTGACGATGACACCTCCTCAGAACTGCAGAGGCTGGC 180
 35 S S R P H S A A D D D T S S E L Q R L A 54
 181 AGACGTGGATGCCCCACAGCAGGGAAGGAGTGGCTTCCGCAGGATAGTTGCGCTGGTGGG 240
 55 D V D A P Q Q G R S G F R R I V R L V G 74
 241 GATCATCAGAGAATGGGCCAACAAGAATTTCCGAGAGGAGGAACCTAGGCCTGACTCATT 300
 75 I I R E W A N K N F R E E E P R P D S F 94
 301 CCTCGAGCGTTTTTCGTGGGCTGAACTCCAGACTGTGACCACACAGGAGGGGATGGCAA 360
 95 L E R F R G P E L Q T V T T Q E G D G K 114
 361 AGGCGACAAGGATGGCGAGGACAAAGGCACCAAGAAGAAATTTGAACTATTTGTCTTGGA 420
 115 G D K D G E D K G T K K K F E L F V L D 134
 421 CCCAGCTGGGGATTTGTACTACTGCTGGCTATTGTGCTATTGCCATGCCCCGCTCTTTACAA 480
 135 P A G D L Y Y C W L F V I A M P V L Y N 154
 481 CTGGTGCCTGTGGTGGCCAGAGCCTGCTTCAGTGACCTACAGAAAGGCTACTACCTGGT 540
 155 W C L L V A R A C F S D L Q K G Y Y L V 174
 541 GTGGCTGGTGTGGATTATGTCTCAGATGTGGTCTACATTGCGGACCTCTTCATCCGATT 600
 175 W L V L D Y V S D V V Y I A D L F I R L 194
 601 GCGCACAGGTTTCTGAGCAGGGGCTGCTGGTCAAAGATACCAAGAACTGCGAGACAA 660
 195 R T G F L E Q G L L V K D T K K L R D N 214
 661 CTACATCCACACCCTGCAGTTCAAGCTGGATGTGGCTTCCATCATCCCCACTGACCTGAT 720
 215 Y I H T L Q F K L D V A S I I P T D L I 234
 721 CTATTTTGCTGTGGACATCCACAGCCCTGAGGTGCGCTTCAACCGCTGCTGCACTTTGC 780
 235 Y F A V D I H S P E V R F N R L L H F A 254
 781 CCGCATGTTTGAGTTCTTTGACCGACAGAGACACGCACCAACTACCCTAACATCTTCCG 840
 255 R M F E F F D R T E T R T N Y P N I F R 274
 841 CATCAGCAACCTTGTCTCTACATCTTGGTCATCATCCACTGGAATGCCTGCATCTATTA 900
 275 I S N L V L Y I L V I I H W N A C I Y Y 294
 901 TGCCATCTCCAAATCCATAGGCTTTGGGGTCGACACCTGGGTTTACCCAAACATCACTGA 960
 295 A I S K S I G F G V D T W V Y P N I T D 314

FIG. 5 (Cont'd)

961 CCCTGAGTATGGCTACCTGGCTAGGGAATACATCTATTGCCTTTACTGGTCCACACTGAC 1020
 315 P E Y G Y L A R E Y I Y C L Y W S T L T 334

1021 TCTCACTACCATTGGGGAGACACCAACCCCTGTAAAGGATGAGGAGTACCTATTGTTCAT 1080
 335 L T T I G E T P P P V K D E E Y L F V I 354

1081 CTTTGACTTCCTGATTGGCGTCCTCATCTTTGCCACCATCGTGGGAAATGTGGGCTCCAT 1140
 355 F D F L I G V L I F A T I V G N V G S M 374

1141 GATCTCCAACATGAATGCCACCCGGGCAGAGTTCAGGCTAAGATCGATGCCGTGAAACA 1200
 375 I S N M N A T R A E F Q A K I D A V K H 394

1201 CTACATGCAGTTCCGAAAGGTGAGCAAGGGGATGGAAGCCAAGGTCATTAGGTGGTTTGA 1260
 395 Y M Q F R K V S K G M E A K V I R W F D 414

1261 CTACTTGTGGACCAATAAGAAGACAGTGGATGAGCGAGAAATTCTCAAGAATCTGCCAGC 1320
 415 Y L W T N K K T V D E R E I L K N L P A 434

1321 CAAGCTCAGGGCTGAGATAGCCATCAATGTCCACTTGTCCACACTCAAGAAAGTGCAT 1380
 435 K L R A E I A I N V H L S T L K K V R I 454

1381 CTTCCATGATTGTGAGGCTGGCCTGCTGGTAGAGCTGGTACTGAAACTCCGTCCTCAGGT 1440
 455 F H D C E A G L L V E L V L K L R P Q V 474

1441 CTCAGTCCTGGGGATTACATTTGCCGCAAAGGGGACATCGGCAAGGAGATGTACATCAT 1500
 475 F S P G D Y I C R K G D I G K E M Y I I 494

1501 TAAGGAGGGCAAAGTGGCAGTGGTGGCTGATGATGGTGTGACTCAGTATGCTCTGCTGTC 1560
 495 K E G K L A V V A D D G V T Q Y A L L S 514

1561 GGCTGGAAGCTGCTTTGGCGAGATCAGTATCCTTAACATTAAGGGCAGTAAAATGGGCAA 1620
 515 A G S C F G E I S I L N I K G S K M G N 534

1621 TCGACGCACAGCTAATATCCGCAGCCTGGGCTACTCAGATCTTCTGCTTGTCCAAGGA 1680
 535 R R T A N I R S L G Y S D L F C L S K D 554

1681 TGATCTTATGGAAGCTGTGACTGAGTACCCTGATGCCAAGAAAGTCTAGAAAGAGAGGGG 1740
 555 D L M E A V T E Y P D A K K V L E E R G 574

1741 TCGGGAGATCCTCATGAAGGAGGGGACTGCTGGATGAGAACGAAGTGGCAACCAGCATGGA 1800
 575 R E I L M K E G L L D E N E V A T S M E 594

1801 GGTGACGTCAGGAGAAGCTAGGGCAGCTGGAGACCAACATGGAACCTTGTACACTCG 1860
 595 V D V Q E K L G Q L E T N M E T L Y T R 614

1861 CTTTGGCCGCTGCTGGCTGAGTACACGGGGGCCAGCAGAAGCTCAAGCAGCGCATCAC 1920
 615 F G R L L A E Y T G A Q Q K L K Q R I T 634

FIG. 5 (Cont'd)

1921 AGTTCTGGAAACCAAGATGAAACAGAACAATGAAGATGACTACCTGTCTGATGGGATGAA 1980
635 V L E T K M K Q N N E D D Y L S D G M N 654

1981 CAGCCCTGAGCTGGCTGCTGCTGACGAGCCATAAGACCTGGGGCCCAACTGCCTCTCCAG 2040
655 S P E L A A A D E P 664

2041 CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTAGATCTCCGGATTACAT 2100

2101 GCATTACCCTCATGTTCCCTGAATTCTCCAAAAGCCTCTCTGACCCTGGGTTTTTGCC 2160

2161 TAAACATCCAAGATTCCGCCTCGGATCCCG 2190

1921 AGTTCTGGAAACCAAGATGAAACAGAACAATGAAGATGACTACCTGTCTGATGGGATGAA 1980
635 V L E T K M K Q N N E D D Y L S D G M N 654

1981 CAGCCCTGAGCTGGCTGCTGCTGACGAGCCATAAGACCTGGGGCCCAACTGCCTCTCCAG 2040
655 S P E L A A A D E P 664

2041 CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTAGATCTCCGGATTACAT 2100

2101 GCATTACCCTCATGTTCCCTGAATTCTCCAAAAGCCTCTCTGACCCTGGGTTTTTGCC 2160

2161 TAAACATCCAAGATTCCGCCTCGGATCCCG 2190

FIG. 6

MTEKTNGVKSSPANNHNNHHAPPAIKANGKDDHRTSSRPHTSAADDDTSSELQRLADVDAPOQGRSGFRRI
VRLVGIIREWANKNFREEPRPDSFLERFRGPELQTVTTQEGDGKGDGDGEDKGTKKKFELFVLDPAGD
LYYCWLFIAMPVLYNWCLLVARACFSDLQKGYLVWLVDYVSDVVIADLFIRLRTGFLEQGGLLVKD
TKKLRDNYIHTLQFKLDVASIIPDLDIYFAVDIHSPEVRFNRLLHFARMFEFFDRTETRTNYPNIFRIS
NLVLYILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTTLTTIGETPPP
KDEEYLFVIFDFLIGVLIFATIVGNVGSISMNMNATRAEFQAKIDAVKHVMQFRKVSKEAKVIRWFD
YLWNTNKTVDEREILKNLPAKLRAEIAINVHLSTLKKVRI FHDCEAGLLVELVLKLRPQVFSPGDYICR
KGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKSGKMGNNRTANIRSLGYSDLFCLS
KDDLMEAVTEYPDAAKVLLEERGRIILMKEGLLDENEVATSMEDVDVQEKLGQLETNMETLYTRFGRLAE
YTGAQQKLKQRITVLETKMKQNNEDDYLSDGMNSPELAADEP

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1 MTEKTNGVKSSPANNHNHHAPPAIKANGKDDHRTSSRPHSAADDDTSSEL 50
1 MTEKTNGVKSSPANNHNHHAPPAIKANGKDDHRTSSRPHSAADDDTSSEL 50

51 QRLADVDAPQQGRSGFRRIVRLVGIIREWANKNFREEEPRPDSFLERFRG 100
51 QRLADVDAPQQGRSGFRRIVRLVGIIREWANKNFREEEPRPDSFLERFRG 100

101 PELQTVTTQEGDGKGDKDGEDKGTKKKKFELFVLDPAGDLYYCWLFIAMP 150
101 PELQTVTTQEGDGKGDKDGEDKGTKKKKFELFVLDPAGDLYYCWLFIAMP 150

151 VLYNWCLLVARACFSDLQKGYLLVWLVLVDYVSDVVIYIADLFIRLRTGFLE 200
151 VLYNWCLLVARACFSDLQKGYLLVWLVLVDYVSDVVIYIADLFIRLRTGFLE 200

201 QGLLVKDTKKLRDNYIHTLQFKLDVASIIPDCLIYFAVDIHSPEVRFNRL 250
201 QGLLVKDTKKLRDNYIHTLQFKLDVASIIPDCLIYFAVDIHSPEVRFNRL 250

251 LHFARMFEFFDRTESTRNYPNIFRISNLVLYILVLIHWNACIYYAISKSI 300
251 LHFARMFEFFDRTESTRNYPNIFRISNLVLYILVLIHWNACIYYAISKSI 300

301 GFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTIGETPPPVKDEEY 350
301 GFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTIGETPPPVKDEEY 350

351 LFVIFDFLIGVLIFATIVGNVGSISMNATRAEFQAKIDAVKHYMQFRK 400
351 LFVIFDFLIGVLIFATIVGNVGSISMNATRAEFQAKIDAVKHYMQFRK 400

401 VSKGMEAKVIRWFDYLWTNKKTVDEREILKNLPAKLRAEIAINVHLSTLK 450
401 VSKGMEAKVIRWFDYLWTNKKTVDEREILKNLPAKLRAEIAINVHLSTLK 450

451 KVRIFHDCEAGLLVELVLKLRPQVSPGDYICRKGDIGKEMYIIKEGKLA 500
451 KVRIFHDCEAGLLVELVLKLRPQVSPGDYICRKGDIGKEMYIIKEGKLA 500

501 VVADDGVTQYALLSAGSCFGEISILNIKSGSKMGNRRATANIRSLGYSDLFC 550
501 VVADDGVTQYALLSAGSCFGEISILNIKSGSKMGNRRATANIRSLGYSDLFC 550

551 LSKDDLMEAVTEYPDAAKVLEERGRIILMKEGLLDENEVATSMEVDVQEK 600
551 LSKDDLMEAVTEYPDAAKVLEERGRIILMKEGLLDENEVATSMEVDVQEK 600

601 LGQLETNMETLYTRFGRLLAEYTGAAQQLKQKITVLETMKMQNNEDDYL 650
601 LGQLETNMETLYTRFGRLLAEYTGAAQQLKQKITVLETMKMQNNEDDYL 650

651 DGMNSPELAAADEP* 665
651 DGMNSPELAAADEP. 664

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